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SERIAL NUMBER 08/813 323	FILED DATE 3/10/97	FIRST NAMED APPLICANT BALTIMORE	ATTORNEY DOCKET NO. 50659/JPW/JM
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JOHN P WHITE
COOPER AND DUNHAM
1185 AVENUE OF THE AMERICAS
NEW YORK NY 10036

18M1/1112

RECEIVED
COOPER & DUNHAM

NOV 14 1997

EXAMINER	
EYLER, Y Yvonne Eyler, Ph.D.	
ART UNIT	PAPER NUMBER
1806	1806

DATE MAILED:

11/12/97

12/12/97

Please find below a communication from the **EXAMINER** in charge of this application
Commissioner of Patents

The communication filed on 8/04/97 is not fully responsive to the communication mailed 5/30/97 for the reasons set forth on the attached Notice to Comply with the Sequence Rules or CRF Diskette Problem Report.

Since the response appears to be bona fide, but through an apparent oversight or inadvertence failed to provide a complete response, Applicant is required to complete the response within a time limit of one (1) month from the date of this letter or within the time remaining in the response period of the communication mailed 5/30/97, whichever is the longer. 37 C.F.R. 1.135 (c).

Any inquiry concerning this communication should be directed to Examiner Yvonne Eyler, Art Unit 1806, whose telephone number is (703) 308-6564.

Any inquiry of a general nature or relating to the status of this application should be directed to the Group receptionist whose telephone number is (703) 308-0196.

Any questions regarding compliance with the sequence rules requirements specifically should be directed to the departments listed at the bottom of the Notice to Comply.

NO EXTENSION OF TIME LIMIT MAY BE GRANTED UNDER EITHER 37 C.F.R. 1.136 (a) OR (b), BUT THE STATUTORY PERIOD FOR RESPONSE SET IN THE COMMUNICATION MAILED 6/7/96 MAY BE EXTENDED UP TO A MAXIMUM OF SIX (6) MONTHS UNDER 37 C.F.R. 1.136.

Any inquiry concerning this communication or earlier communications from the examiner should be directed to Yvonne Eyler, Ph.D. whose telephone number is (703) 308-6564. The examiner can normally be reached on Monday through Friday from 830am to 630pm.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Lila Feisee, can be reached on (703) 308-2731. The fax phone number for this Group is (703) 305-3014 or (703) 308-4242.

Communications via Internet e-mail regarding this application, other than those under 35 U.S.C. 132 or which otherwise require a signature, may be used by the applicant and should be addressed to [lila.feisee@uspto.gov].

All Internet e-mail communications will be made of record in the application file. PTO employees do not engage in Internet communications where there exists a possibility that sensitive information could be

identified or exchanged unless the record includes a properly signed express waiver of the confidentiality requirements of 35 U.S.C. 186. This is more clearly set forth in the Interim Internet Usage Policy published in the Official Gazette of the Patent and Trademark on February 25, 1997 at 1195 OG 89.

Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the Group receptionist whose telephone number is (703) 308-0196.

11/10/97

Yvonne Eyler, Ph.D.



LILA FEISZE
SUPERVISORY PATENT EXAMINER
GROUP 1800

Application No. 08/813,323

**NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING
NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES**

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 CFR 1.821 - 1.825 for the following reason(s):

- ☐ 1. This application clearly fails to comply with the requirements of 37 CFR 1.821 - 1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29 May 15, 1990 and at 55 FR 18230, May 1, 1990.
- ☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 CFR 1.821(c).
- ☐ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 CFR 1.821(e).
- ☒ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked-up "Raw Sequence Listing."
- ☒ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A substitute computer readable form must be submitted as required by 37 CFR 1.825(d).
- ☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable form of the "Sequence Listing" as required by 37 CFR 1.821(e).
- ☐ 7.

Other: _____

Applicant must provide:

- ☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing"
- ☒ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification
- ☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 CFR 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d)

For questions regarding compliance with these requirements, please contact

For Rules Interpretation, call (703) 308-1123

For CRF submission help, call (703) 308-4212

For PatentIn software help, call (703) 557-0400

Please return a copy of this notice with your response.

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following CRF diskette:

Application Serial Number:

08/813323

Filing Date:

3/10/97

Classification:

530

Date Processed by STIC:

9/10/97

Point-of-Contact/Telephone No.: Arti Shah 703 - 308 - 4212

Nature of Problem:

The diskette was:

☐ Damaged

☐ Unreadable

☐ Blank (no files present on diskette)

☐ Contained an empty file (filename present, but no bytes in file)

☐ A computer virus was detected on the diskette. The STIC will not process the diskette through the Data Capture System.

Name of virus: _____

☒ The Sequence Listing was not saved in ASCII (DOS) text.

☐ The diskette contained an error that disrupted normal processing:



-40-

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Baltimore, David
Cheng, Genhong
Cleary, Aileen
Lederman, Seth
Ye, Zheng-sheng
- (ii) TITLE OF INVENTION: TRUNCATED CRAF1 INHIBITS CD40 SIGNALING
- (iii) NUMBER OF SEQUENCES: 5
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Cooper & Dunham, LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10036
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: White, John P
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 50659
- (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: (212) 278-0400
(B) TELEFAX: (212) 391-0525

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 566 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..566

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met Glu Ser Ser Lys Lys Met Asp Ala Ala Gly Thr Leu Gln Pro Asn
1 5 10 15
Pro Pro Leu Lys Leu Gln Pro Asp Arg Gly Ala Gly Ser Val Leu Val
20 25 30
Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu Asp
35 40 45
Lys Tyr Lys Cys Glu Lys Cys Arg Leu Val Leu Cys Asn Pro Lys Gln
50 55 60
Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu Leu
65 70 75 80
Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Ile Lys
85 90 95
Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala Leu
100 105 110
Gln Val Tyr Cys Arg Asn Glu Gly Arg Gly Cys Ala Glu Gln Leu Thr
115 120 125
Leu Gly His Leu Leu Val His Leu Lys Asn Glu Cys Gln Phe Glu Glu
130 135 140
Leu Pro Cys Leu Arg Ala Asp Cys Lys Glu Lys Val Leu Arg Lys Asp
145 150 155 160
Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr Cys
165 170 175
Ser His Cys Lys Ser Gln Val Pro Met Ile Lys Leu Gln Lys His Glu
180 185 190
Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys Ser
195 200 205
Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu Cys
210 215 220
Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val Phe
225 230 235 240
Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala Val
245 250 255
Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys Lys
260 265 270
Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile Gln
275 280 285

Ab
T2
m
T1

Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg Gln
 290 295 300

Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln Arg
 305 310 315 320

Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu Ile
 325 330 335

Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser Ser
 340 345 350

Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp Lys
 355 360 365

Ser Ala Gly Gln Ala Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln Leu
 370 375 380

Ser Arg His Asp Gln Thr Leu Ser Val His Asp Ile Arg Leu Ala Asp
 385 390 395 400

Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly Val
 405 410 415

Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala Val
 420 425 430

Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly Tyr
 435 440 445

Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly Met
 450 455 460

Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly Glu
 465 470 475 480

Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu Met
 485 490 495

Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe Lys
 500 505 510

Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met Asn
 515 520 525

Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu Asn
 530 535 540

Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val Asp
 545 550 555 560

Thr Ser Asp Leu Pro Asp
 565

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 568 amino acids

(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Peptide
(B) LOCATION: 1..568

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Glu Ser Ser Lys Lys Met Asp Ser Pro Gly Ala Leu Gln Thr Asn
1 5 10 15
Pro Pro Leu Lys Leu His Thr Asp Arg Ser Ala Gly Thr Pro Val Phe
20 25 30
Val Pro Glu Gln Gly Gly Tyr Lys Glu Lys Phe Val Lys Thr Val Glu
35 40 45
Asp Lys Tyr Lys Cys Glu Lys Cys His Leu Val Leu Cys Ser Pro Lys
50 55 60
Gln Thr Glu Cys Gly His Arg Phe Cys Glu Ser Cys Met Ala Ala Leu
65 70 75 80
Leu Ser Ser Ser Ser Pro Lys Cys Thr Ala Cys Gln Glu Ser Ile Val
85 90 95
Lys Asp Lys Val Phe Lys Asp Asn Cys Cys Lys Arg Glu Ile Leu Ala
100 105 110
Leu Gln Ile Tyr Cys Arg Asn Glu Ser Arg Gly Cys Ala Glu Gln Leu
115 120 125
Thr Leu Gly His Leu Leu Val His Leu Lys Asn Asp Cys His Phe Glu
130 135 140
Glu Leu Pro Cys Val Arg Pro Asp Cys Lys Glu Lys Val Leu Arg Lys
145 150 155 160
Asp Leu Arg Asp His Val Glu Lys Ala Cys Lys Tyr Arg Glu Ala Thr
165 170 175
Cys Ser His Cys Lys Ser Gln Val Pro Met Ile Ala Leu Gln Lys His
180 185 190
Glu Asp Thr Asp Cys Pro Cys Val Val Val Ser Cys Pro His Lys Cys
195 200 205
Ser Val Gln Thr Leu Leu Arg Ser Glu Leu Ser Ala His Leu Ser Glu
210 215 220
Cys Val Asn Ala Pro Ser Thr Cys Ser Phe Lys Arg Tyr Gly Cys Val
225 230 235 240

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12/1

71

Phe Gln Gly Thr Asn Gln Gln Ile Lys Ala His Glu Ala Ser Ser Ala
 245 250 255
 Val Gln His Val Asn Leu Leu Lys Glu Trp Ser Asn Ser Leu Glu Lys
 260 265 270
 Lys Val Ser Leu Leu Gln Asn Glu Ser Val Glu Lys Asn Lys Ser Ile
 275 280 285
 Gln Ser Leu His Asn Gln Ile Cys Ser Phe Glu Ile Glu Ile Glu Arg
 290 295 300
 Gln Lys Glu Met Leu Arg Asn Asn Glu Ser Lys Ile Leu His Leu Gln
 305 310 315 320
 Arg Val Ile Asp Ser Gln Ala Glu Lys Leu Lys Glu Leu Asp Lys Glu
 325 330 335
 Ile Arg Pro Phe Arg Gln Asn Trp Glu Glu Ala Asp Ser Met Lys Ser
 340 345 350
 Ser Val Glu Ser Leu Gln Asn Arg Val Thr Glu Leu Glu Ser Val Asp
 355 360 365
 Lys Ser Ala Gly Gln Val Ala Arg Asn Thr Gly Leu Leu Glu Ser Gln
 370 375 380
 Leu Ser Arg His Asp Gln Met Leu Ser Val His Asp Ile Arg Leu Ala
 385 390 395 400
 Asp Met Asp Leu Arg Phe Gln Val Leu Glu Thr Ala Ser Tyr Asn Gly
 405 410 415
 Val Leu Ile Trp Lys Ile Arg Asp Tyr Lys Arg Arg Lys Gln Glu Ala
 420 425 430
 Val Met Gly Lys Thr Leu Ser Leu Tyr Ser Gln Pro Phe Tyr Thr Gly
 435 440 445
 Tyr Phe Gly Tyr Lys Met Cys Ala Arg Val Tyr Leu Asn Gly Asp Gly
 450 455 460
 Met Gly Lys Gly Thr His Leu Ser Leu Phe Phe Val Ile Met Arg Gly
 465 470 475 480
 Glu Tyr Asp Ala Leu Leu Pro Trp Pro Phe Lys Gln Lys Val Thr Leu
 485 490 495
 Met Leu Met Asp Gln Gly Ser Ser Arg Arg His Leu Gly Asp Ala Phe
 500 505 510
 Lys Pro Asp Pro Asn Ser Ser Ser Phe Lys Lys Pro Thr Gly Glu Met
 515 520 525
 Asn Ile Ala Ser Gly Cys Pro Val Phe Val Ala Gln Thr Val Leu Glu
 530 535 540

Amb
 T24

71

Asn Gly Thr Tyr Ile Lys Asp Asp Thr Ile Phe Ile Lys Val Ile Val
545 550 555 560
Asp Thr Ser Asp Leu Pro Asp Pro
565

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 2359 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCGGCGGAG GATGCGCGCG GCGCCTGAGC CGGCCGAACG GGCGGCCTCG GGGTACAGGG 60
TCCCCATTAC TTGAAGGATA AGGCTGGCAC GGCTCCGACG TCTGTGTGGA AGCTTCTCCC 120
TCCCTTCTGA GCTTCTCTAG ACTCCTTACA GCGCACGGCA CAGAATTTCA GTTTCCTAAG 180
ATGGAGTCAA GCAAAAAGAT GGATGCTGCT GGCACACTGC AGCCTAACCC ACCCCTAAAG 240
CTGCAGCCTG ATCGCGGCGC AGGGTCCGTG CTGTGCGCGG AGCAAGGAGG CTACAAGGAG 300
AAGTTTGTGA AGACGGTGGA AGACAAGTAC AAGTCCGAGA AGTGCCGCCT GGTGCTGTGC 360
AACCCGAAGC AGACGGAGTG TGGCCACCGG TTCTGCGAGA GCTGCATGGC CGCCCTGCTG 420
AGCTCCTCCA GTCCAAAATG CACAGCGTGC CAAGAAAGCA TCATCAAAGA CAAGGTGTTT 480
AAGGATAATT GCTGCAAGAG AGAGATTCTG GCCCTTCAGG TCTACTGTCTG GAATGAAGGC 540
AGAGGTTGTG CGGAGCAGCT GACTCTGGGA CATCTGCTGG TGCACCTAAA AAATGAATGT 600
CAGTTTGAGG AACTTCCCTG TCTGCGTGCC GACTGCAAAG AAAAAGTACT GAGAAAAGAC 660
TTGCGGGATC ACGTGGA AAA GGCCTGTAAA TACCGCGAGG CCACGTGCAG TCACTGCAAG 720
AGCCAAGTGC CCATGATCAA ACTGCAGAAA CATGAAGACA CAGATTGTCC CTGTGTGGTG 780
GTATCCTGCC CTCACAAGTG CAGCGTTCAG ACTCTTCTAA GGAGTGAGTT GAGTGCACAC 840
TTGTCCGAGT GTGTCAATGC CCCAGCACC TGTAGTTTTA AGCGCTATGG CTGCGTTTTT 900
CAGGGTACAA ACCAGCAGAT CAAGGCCCAT GAGGCCAGCT CCGCGGTACA GCACGTGAAC 960
CTGCTGAAGG AGTGGAGCAA CTCCCTGGAG AAGAAGGTTT CCCTGCTGCA GAATGAAAGT 1020
GTTGAGAAAA ACAAGAGCAT CCAAAGCCTG CACAACCAGA TCTGCAGCTT TGAGATCGAG 1080
ATTGAGAGGC AGAAGGAGAT GCTCCGAAAC AACGAGTCCA AGATCCTTCA CCTGCAGCGG 1140

GTAATCGACA GCCAAGCAGA GAAACTGAAA GAACTGGACA AGGAGATCCG TCCCTTCCGG 1200
 CAGAACTGGG AGGAAGCGGA CAGCATGAAG AGCAGTGTGG AGTCCCTCCA GAACCGAGTG 1260
 ACTGAGCTGG AGAGCGTAGA CAAAAGTGCG GGGCAGGCGG CTCGCAACAC AGGCTTGCTG 1320
 GAGTCCCAGC TGAGCCGGCA TGACCAGACG TTGAGTGTTC ATGACATCCG CTTGGCCGAC 1380
 ATGGACCTGC GGTTCAGGT CCTCGAGACC GCCAGCTACA ACGGGGTGCT GATCTGGAAG 1440
 ATCCGTGACT ACAAGCGCGG GAAGCAGGAG GCCGTCATGG GGAAGACCCT GTCTCTCTAC 1500
 AGCCAGCCTT TCTACACAGG TTATTTTGGC TATAAGATGT GTGCCAGGGT CTACCTGAAT 1560
 GGGGACGGAA TGGGGAAAGG GACACACTTG TCGCTGTTTT TTGTCATTAT GCGTGAGAGAA 1620
 TATGATGCTC TGTTGCCATG GCGGTTCAAG CAGAAAGTGA CACTTATGCT GATGGATCAG 1680
 GGGTCCTCTC GCCGTCATCT GGGAGATGCG TTCAAGCCTG ACCCCAACAG CAGCAGCTTC 1740
 AAGAAACCCA CCGGAGAGAT GAATATCGCC TCTGGCTGCC CAGTCTTTGT CGCCCAAAC 1800
 GTTCTAGAGA ACGGGACGTA TATTAAAGAT GATACAATCT TTATTAAGGT CATAGTGGAT 1860
 ACCTCGGATC TGCCTGACCC CTGACAAGAA AGCAGGGCGG TGGATTGAGC AGAAGGTAAC 1920
 TCCTCTGGGG GGGTGAGCTA GTGTCTTCAC GGAGGTCCTC GCCCTCAGAA AGGACCTTGT 1980
 GGCGCAGAGG AAGCAGCCGG AGGAGGAGAA GGAGGTCGAG TGGCTGGCAG GAGAGCCACA 2040
 TGTGAAAACA GACCCCAACG GATTTTCTAA TAAAGTAGCC ACACCCACTC TGAAGGATTA 2100
 TTTATCCATC AACAAAGATAA ATACTGCTGT CAGAGAAAGT TTTTATTTTC ATTTTAAAAG 2160
 ATCTAGTATT AAGGTGGGAA CATATATGCT AAAAAGAAAC ATGATTTTTC TTCCTTAACT 2220
 TAAACACCAA AAAGAGAACA CATGTGGGGG TAGCTGGAGT GTGTACAGTA CCTCGAGGGC 2280
 TTAAATCAT AAACAATCAC ATACTCATCC TAAATTCAG GGTGCAACTC CGTTTCAAAT 2340
 ATTGTATATT GTCTATTTA 2359

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2455 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGGGAGCG CGGCGCGGCC GCCGCGTGCG CGAGCCGGGG TTGCAGCCCA GCCGGGACTT

TCCAGCCGGC GGCAGCCGCG GCGGTCGTCG GCTCTTCCCC GCGGCGGTC ATGGGGCAGC 120
CCGGGGAGCA GAACGCTGCG GACCGCGGCG GAGGACGCGC CCGGCGCCCC TGAGCCGGCC 180
GAGCGGCGAC GGACGCGGAG AACTCCTCTT TCCTAAAATG GAGTCGAGTA AAAAGATGGA 240
CTCTCCTGGC GCGCTGCGA CTAACCCGCC GCTAAAGCTG CACACTGACC GTAGTGCTGG 300
GACGCCAGTT TTTGTCCCTG AACAAGGAGG TTACAAGGAA AAGTTTGTGA AGACCGTGGA 360
GGACAAGTAC AAGTGTGAGA AGTGCCACCT GGTGCTGTGC AGCCCGAAGC AGACCGAGTG 420
TGGGCACCGC TTCTGCGAGA GCTGCATGGC GGCCCTGCTG AGCTCTTCAA GTCCAAAATG 480
TACAGCGTGT CAAGAGAGCA TCCTTAAAGA TAAGGTGTTT AAGGATAATT GCTGCAAGAG 540
AGAAATTCTG GCTCTTCAGA TCTATTGTCG GAATGAAAGC AGAGGTTGTG CAGAGCAGTT 600
AACGCTGGGA CATCTGCTGG TGCATTTAAA AAATGATTGC CATTTTGAAG AACTTCCATG 660
TGTGCGTCCT GACTGCAAAG AAAAGGTCTT GAGGAAAGAC CTGCGAGACC ACGTGGAGAA 720
GGCGTGTAAT TACCGGGAAG CCACATGCAG CCACTGCAAG AGTCAGGTTT CGATGATCGC 780
GCTGCAGAAA CACGAAGACA CCGACTGTCC CTGCGTGGTG GTGTCCTGCC CTCACAAGTG 840
CAGCGTCCAG ACTCTCCTGA GGAGCGAGTT GAGTGACAC TTGTCAGAGT GTGTCAATGC 900
CCCCAGCACC TGCTAGTTTTA AGCGCTATGG CTGCGTTTTT CAGGGGACAA ACCAGCAGAT 960
CAAGGCCCCAC GAGGCCAGCT CCGCCGTGCA GCACGTCAAC CTGCTGAAGG AGTGGAGCAA 1020
CTCGCTCGAA AAGAAGGTTT CCTTGTTGCA GAATGAAAGT GTAGAAAAAA ACAAGAGCAT 1080
ACAAAGTTTG CACAATCAGA TATGTAGCTT TGAAATTGAA ATTGAGAGAC AAAAGGAAAT 1140
GCTTCGAAAT AATGAATCCA AAATCCTTCA TTTACAGCGA GTGATCGACA GCCAAGCAGA 1200
GAAACTGAAG GAGCTTGACA AGGAGATCCG GCCCTTCCGG CAGAACTGGG AGGAAGCAGA 1260
CAGCATGAAG AGCAGCGTGG AGTCCCTCCA GAACCGCGTG ACCGAGCTGG AGAGCGTGGA 1320
CAAGAGTGCG GGGCAAGTGG CTCGGAACAC AGGCCTGCTG GAGTCCCAGC TGAGCCGGCA 1380
TGACCAGATG CTGAGTGTGC ACGACATCCG CCTAGCCGAC ATGGACCTGC GCTTCCAGGT 1440
CCTGGAGACC GCCAGCTACA ATGGAGTGCT CATCTGGAAG ATTCGCGACT ACAAGCGGCG 1500
GAAGCAGGAG GCCGTCATGG GGAAGACCCT GTCCCTTTAC AGCCAGCCTT TCTACACTGG 1560
TTACTTTGGT TATAAGATGT GTGCCAGGGT CTACCTGAAC GGGGACGGGA TGGGGAAGGG 1620
GACGCACTTG TCGCTGTTTT TTGTCATCAT GCGTGGAGAA TATGATGCCC TGCTTCCTTG 1680
GCCGTTTAAG CAGAAAGTGA CACTCATGCT GATGGATCAG GGGTCCTCTC GACGTCATTT 1740
GGGAGATGCA TTCAAGCCCG ACCCCAACAG CAGCAGCTTC AAGAAGCCCA CTGGAGAGAT 1800

GAATATCGCC TCTGGCTGCC CAGTCTTTGT GGCCCAAAC GTTCTAGAAA ATGGGACATA 1860
TATTAAAGAT GATACAATTT TTATTAAAGT CATAGTGGAT ACTTCGGATC TGCCCGATCC 1920
CTGATAAGTA GCTGGGGAGG TGGATTTAGC AGAAGGCAAC TCCTCTGGGG GATTTGAACC 1980
GGTCTGTCTT CACTGAGGTC CTCGCGCTCA GAAAAGGACC TTGTGAGACG GAGGAAGCGG 2040
CAGAAGGCGG ACGCGTGCGG GCGGGAGGAG CCACGCGTGA GCACACCTGA CACGTTTTAT 2100
AATAGACTAG CCACACTTCA CTCTGAAGAA TTATTTATCC TTCAACAAGA TAAATATTGC 2160
TGTCAGAGAA GGTTTTCATT TTCATTTTAA AAGATCTAGT TAATTAAGGT GGAAAACATA 2220
TATGCTAAAC AAAAGAAACA TGATTTTCT TCCTTAAACT TGAACACCAA AAAACACAC 2280
ACACACACAC ACGTGGGGAT AGCTGGACAT GTCAGCATGT TAAGTAAAAG GAGAATTTAT 2340
GAAATAGTAA TGCAATTCTG ATATCTTCTT TCTAAAATTC AAGAGTGCAA TTTTGTTTCA 2400
AATACAGTAT ATTGTCTATT TTTAAGGCCT CCAAAAAAAA AAAAAATTCC GGCCG 2455

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Lys Ala Cys Lys Tyr Arg
1 5

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Applicant : David Baltimore, et al.
Serial No. : 08/813,323
Filed : March 10, 1997 Art Unit: 1815
For : TRUNCATED CRAF1 INHIBITS CD40 SIGNALING

1185 Avenue of the Americas
New York, New York 10036
November 25, 1997

Assistant Commissioner for Patents
Washington, D.C. 20231

ATTENTION: BOX SEQUENCE

SIR:

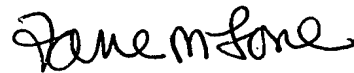
STATEMENT IN ACCORDANCE WITH 37 C.F.R. §1.821(f)

In accordance with 37 C.F.R. §1.821(f), I hereby certify that the computer readable form containing the nucleic acid and/or amino acid sequences required by 37 C.F.R. §1.821(f) and submitted in connection with the above-identified application, has the same content as that submitted on pages 40-48 entitled "Sequence Listing," attached hereto as Exhibit B.

David Baltimore, et al.
U.S. Serial No.: 08/813,323
Filed: March 10, 1997
Page 2

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

Respectfully submitted,



Jane M. Love
c/o Cooper & Dunham LLP
1185 Avenue of the Americas
New York, New York 10036
(212) 278-0400